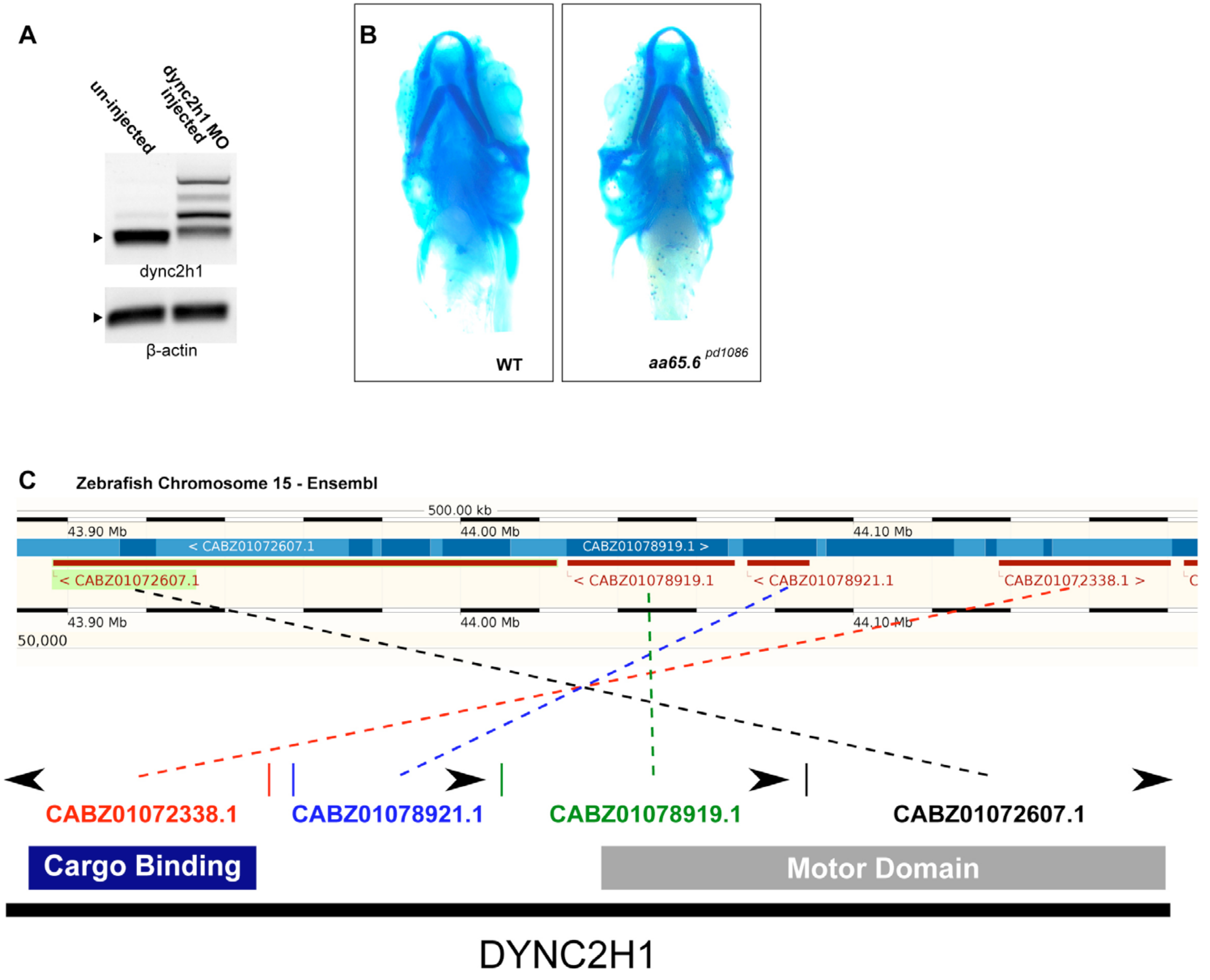

Fig. S1. *dync2h1* morpholino validation and supplemental characterization of *aa65.6*^{pd1086} mutant. **(A)** RT-PCR from RNA of control and *dync2h1* splice-site morpholino-injected EK embryos at the one cell stage and harvested at 3 dpf. **(B)** Ventral view of cartilage in the jaw of 5 dpf alcian-blue stained larvae. **(C)** View of chromosome 15 in Ensembl showing the four transcripts that constitute the full length *dync2h1* in zebrafish and the corresponding protein domains.

Table S1. Whole exome capture and Illumina HiSeq 2x100 bp sequencing coverage statistics for each WT/MUT pool

Sample	Total paired-end reads	% Reads mapped to genome	% Bases covering Ensgene	Mean base quality	% TARGET BASES_20X	Mean target coverage
A-test WT	226.4M	82	69	37	92	230
A-test Mut	190M	82	72	36	92	194
dx36.18 WT	103.5M	86	83	36	94	151
dx36.18 Mut	111M	86	84	36	94	166
aa65.6 WT	31.5M	86	82	36	80	45
aa65.6 Mut	40.5M	87	85	37	87	64
ccn1.9 WT	72M	86	82	36	93	102
ccn1.9 Mut	72M	87	85	37	93	113
dx33.9 WT	125.5M	84	78	37	97	148
dx33.9 Mut	90.5M	84	78	37	94	108

Table S2. Total individuals per WT/MUT pool, linkage interval size in bp and number of SNPs in linkage interval within coding regions

Panel	Individuals in pool	Interval	Total SNPs coding/exon
A-known*	10	8mb	270
36.18**	30	21mb	105
65.6**	30	8.6mb	24
N1.9**	30	27mb	144
DX33.9***	40	17mb	243

Filtered against SNP database, Homo Mut/Het WT only, no reference reads Mut.
*Agilent-SureSelect-Zv9-V1 – 96.7 Mb target region.
**Agilent-SureSelect-Zv9-V2 – 70.6 Mb target region.
***Agilent-SureSelect-Zv9-V1+V2 combined.

Table S3. SNPtrack gene candidate lists for *ccn1.9*^{pd1085}, *dx33.9*^{pd1087}, *dx36.18*^{pd1084} and *aa65.6*^{pd1086}

A. *ccn1.9*^{pd1085} SNPTrack Gene Candidate List

Chr	Position	Ref	Chg	Consequence	Gene	Mutant (WT/MUT)	Wild-Type (WT/MUT)	CDS position	Protein position	Amino acids	Codons
20	37439032	A	C	NON_SYNONYMOUS_CODING	*gpr126*	0/42	19/15	985	329	T/P	Acc/Ccc
20	37464317	C	T	NON_SYNONYMOUS_CODING	*gpr126*	1/127	72/41	1942	648	P/S	Cct/Tct
20	37953087	T	G	NON_SYNONYMOUS_CODING	*angel2*	0/161	87/50	514	172	K/Q	Aag/Cag
20	38128844	C	T	NON_SYNONYMOUS_CODING	*galnt14*	1/101	86/34	1361	454	T/I	aCc/aTc
20	38470717	C	T	NON_SYNONYMOUS_CODING	*itpkb*	1/76	65/32	884	295	G/D	gGt/gAt
20	38593652	T	C	NON_SYNONYMOUS_CODING	*gtf3c2*	1/73	62/19	1412	471	L/P	cTg/cCg
20	38856354	T	A	NON_SYNONYMOUS_CODING	*SDR16C5*	1/21	19/9	1013	338	N/I	aAc/aTc
20	38856369	C	T	NON_SYNONYMOUS_CODING	*SDR16C5*	1/19	20/8	998	333	S/N	aGc/aAc
20	38870195	G	A	ESSENTIAL_SPLICE_SITE	*ift172*	0/60	28/20				
20	39266724	C	T	NON_SYNONYMOUS_CODING	*reps1*	1/129	95/31	1144	382	P/S	Cct/Tct
20	40507779	G	C	NON_SYNONYMOUS_CODING	*hsf2*	1/115	57/30	1456	486	P/A	Ccg/Gcg
20	40836434	C	T	NON_SYNONYMOUS_CODING	*chr6orf170*	1/70	40/21	2696	899	S/L	tCa/tTa
20	46590684	C	T	STOP_GAINED	*flvcr2b*	2/53	39/20	1345	449	Q/*	Cag/Tag

B. *dx33.9*^{pd1087}SNPTrack Gene Candidate List

Chr	Position	Ref	Chg	Consequence	Gene	Mutant (WT/MUT)	Wild-Type (WT/MUT)	CDS position	Protein position	Amino acids	Codons
2	42058893	A	G	NON_SYNONYMOUS_CODING	*HELZ2*	0/45	58/30	6586	2196	S/P	Tct/Cct
2	43220781	A	C	STOP_GAINED	*lrrc6*	0/158	137/68	530	177	L/*	tTa/tGa
2	43960797	C	A	NON_SYNONYMOUS_CODING	*gbp3*	0/55	58/33	784	262	H/N	Cac/Aac
2	44712703	C	T	NON_SYNONYMOUS_CODING	*YEATS2*	0/75	74/43	1979	660	T/I	aCa/aTa
2	44899087	G	A	ESSENTIAL_SPLICE_SITE	*ECE2*	1/111	157/54				
2	45039439	G	A	NON_SYNONYMOUS_CODING	*alg3*	0/79	83/34	758	253	S/N	aGc/aAc
2	45204510	C	T	NON_SYNONYMOUS_CODING	*capn10*	0/151	152/66	1516	506	G/S	Ggt/Agt
2	45210040	G	A	NON_SYNONYMOUS_CODING	*capn10*	0/124	92/50	746	249	T/I	aCc/aTc
2	46421628	A	T	NON_SYNONYMOUS_CODING	*GPC6*	0/53	42/19	356	119	Q/L	cAg/cTg

C. *dx36.18*^{pd1084}SNPTrack Gene Candidate List

Chr	Position	Ref	Chg	Consequence	Gene	Mutant (WT/MUT)	Wild-type (WT/MUT)	CDS position	Protein position	Amino acids	Codons
14	22092159	G	A	NON_SYNONYMOUS_CODING	*RNF20*	0/112	62/29	361	121	R/C	Cgc/Tgc
14	24991172	C	A	SPLICE_SITE&INTRONIC	*kif3a*	1/153	90/37				

D. *aa65.6*^{pd1086}SNPTrack Gene Candidate List

Chr	Position	Ref	Chg	Consequence	Gene	Mutant (WT/MUT)	Wild-type (WT/MUT)	CDS position	Protein position	Amino acids	Codons
15	42636786	G	A	NON_SYNONYMOUS_CODING	*NUMA1*	1/38	21/10	1301	434	R/Q	cGa/cAa
15	42636902	G	A	NON_SYNONYMOUS_CODING	*NUMA1*	2/33	20/9	1417	473	E/K	Gag/Aag
15	42782537	G	C	NON_SYNONYMOUS_CODING	*NUMA1*	2/37	35/19	685	229	P/A	Ccg/Gcg
15	43896563	A	T	STOP_GAINED	*dync2h1*	1/30	22/10	4878	1626	C/*	tgT/tgA